

SEQUENCE LISTING

- (1) GENERAL INFORMATION:
- (i) APPLICANT: LI, ET AL.
- (ii) TITLE OF INVENTION: Human G-Protein Coupled Receptors
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI, STEWART & OLSTEIN
- (B) STREET: 6 BECKER FARM ROAD
- (C) CITY: ROSELAND
- (D) STATE: NEW JERSEY
- (E) COUNTRY: USA
- (F) ZIP: 07068
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5 INCH DISKETTE
- (B) COMPUTER: IBM PS/2
- (C) OPERATING SYSTEM: MS-DOS
- (D) SOFTWARE: WORD PERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER:
- (B) FILING DATE: Concurrently
- (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA
- (A) APPLICATION NUMBER: PCT/US95/04079
- (B) FILING DATE: 30 MAR 1995
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: FERRARO, GREGORY D.
- (B) REGISTRATION NUMBER: 36,134
- (C) REFERENCE/DOCKET NUMBER: 325800-379
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 201-994-1700
- (B) TELEFAX: 201-994-1744
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 1713 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
GGCACGAGGT CATTCAACAT TTATTCAACC AAAAATACTA AGTCAGCTCT ATACAAACTA 60
ATGGAAGGAT ACAGCTATGC AAATATAGAA CACTAAAGTG TTACATGACA GATGTATGAG 120
TAGTGAAATG GTGAAAAATC AGACAATGGT CACAGAGTTC CTCCTACTGG GATTTCTCCT 180
GGGCCCAAGG ATTCAGATGC TCCTCTTTGG GCTCTTCTCC CTGTTCTATG TCTTCACCCT 240
GCTGGGGAAT GGGACCATCC TGGGGCTCAT CTCACTGGAC TCCAGACTCC ACACCCCCAT 300
GTACTTCTTC CTCTCACACC TGGCCGTCGT CAACATCGCC TATGCCTGCA ACACAGTGCC 360
CCAGATGCTG GTGAACCTCC TGCATCCAGC CAAGCCCATC TCCTTTGCTG GTTGCATGAC 420
ACTAGACTTT CTCTTTTTGA GTTTTGCACA TACTGAATGC CTCCTGTTGG TGCTGATGTC 480
CTACGATCGG TACGTGGCCA TCTGCCACCC TCTCCGATAT TTCATCATCA TGACCTGGAA 540
AGTCTGCATC ACTCTGGGCA TCACTTCTCTG GACATGTGGC TCCCTCCTGG CTATGGTCCA 600
TGTGAGCCTC ATCCTAAGAC TGCCCTTTTG TGGGCCTCGT GAAATCAACC ACTTCTTCTG 660
TGAAATCCTG TCTGTCTCA GGCTGGCCTG TGCTGATACC TGGCTCAACC AGGTGGTCAT 720
CTTTGAAGCC TGCATGTTCA TCCTGGTGGG ACCACTCTGC CTGGTGCTGG TCTCCTACTC 780
ACACATCCTG GGGGGCATCC TGAGGATCCA GTCTGGGGAG GGCCGCAGAA AGGCCTTCTC 840
CACCTGCTCC TCCCACCTCT GCGTAGTGGG ACTCTTCTTT GGSAGCGCCA TCGTCATGTA 900
CATGGCCCCC AAGTCCCGCC ATCCTGAGGA GCAGCAGAAG GTCCTTTTTT TTATTTTACA 960
GTTCTTTTCA ACCCCGATGC TTAAACCCCC TGATTTACAA CCCTGAGGAA TGTAGAGGGT 1020
CAAGGGTGCC CTCCGAGGAG ACCACTGTGC AARGRAAGTC ATTCTAAGG GGTGTGACAT 1080
TTGAACTGCC AGCCCCAGTT GCCCCGTGGA CTCCTGATGC CCAATTATTG CCTCAACCCA 1140
GAAAAGTTTA CTCCCCTTTA ACTGTGCTTT ACTGACAGAA GGGCAAGCCT TCTCCCGTTT 1200
TTTGCAGATA AAATTTTAGA TGTGTTGCAA TCATTGGGTT TCTAGGAGAT GTGGTTTTAT 1260
CAGACAATTT TTTCTTTTAT TTCACAATTA CTTTAATATC TGTAAAATAA AGAATTATTT 1320
TAAATCATTT TCCCAGTCCC AAAAGTTAAA TACAGGCCAC TTACTTCTTT AACCAAATGA 1380
TATAGTTTGG CTCTGTGTC CCACCCAAAT CTCATGTCAA ATTGTAATCC CCGCATGTCA 1440
GCGGAGGGAC CTGGTGGGAG GTGATTGGAT CATGGGGAGG GATTTCCCCC TTGCTGTTCT 1500
GTTGATAGTG AACGAGTTCT CACGAAATCT GATGGTTTAA AAGTGCAGCA CTTCTCCCTT 1560
TGCTCTCTCT CTCTGCTGT GCCATGGTAA GACGTGCCTT GCTTCCCCTG GTGCTTCCGC 1620
CATGATTGTA CCTTCTCTGA GGCCTCTCCA GCCATGTGGA ACTGTGAGCC AATTAAACTT 1680
CTTTTCTTTA GAAAAA AAAA AAAA AAAA 1713
```

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS  
(A) LENGTH: 296 AMINO ACIDS  
(B) TYPE: AMINO ACID  
(C) STRANDEDNESS:  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Met Ser Ser Glu Met Val Lys Asn Gln Thr Met Val Thr Glu Phe
5 10 15
Leu Leu Leu Gly Phe Leu Leu Gly Pro Arg Ile Gln Met Leu Leu
20 25 30
Phe Gly Leu Phe Ser Leu Phe Tyr Val Phe Thr Leu Leu Gly Asn
35 40 45
Gly Thr Ile Leu Gly Leu Ile Ser Leu Asp Ser Arg Leu His Thr
50 55 60
Pro Met Tyr Phe Phe Leu Ser His Leu Ala Val Val Asn Ile Ala
65 70 75
Tyr Ala Cys Asn Thr Val Pro Gln Met Leu Val Asn Leu Leu His
80 85 90
Pro Ala Lys Pro Ile Ser Phe Ala Gly Cys Met Thr Leu Asp Phe
```

				95					100					105
Leu	Phe	Leu	Ser	Phe	Ala	His	Thr	Glu	Cys	Leu	Leu	Leu	Val	Leu
				110					115					120
Met	Ser	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	Arg	Tyr
				125					130					135
Phe	Ile	Ile	Met	Thr	Trp	Lys	Val	Cys	Ile	Thr	Leu	Gly	Ile	Thr
				140					145					150
Ser	Trp	Thr	Cys	Gly	Ser	Leu	Leu	Ala	Met	Val	His	Val	Ser	Leu
				155					160					165
Ile	Leu	Arg	Leu	Pro	Phe	Cys	Gly	Pro	Arg	Glu	Ile	Asn	His	Phe
				170					175					180
Phe	Cys	Glu	Ile	Leu	Ser	Val	Leu	Arg	Leu	Ala	Cys	Ala	Asp	Thr
				185					190					195
Trp	Leu	Asn	Gln	Val	Val	Ile	Phe	Glu	Ala	Cys	Met	Phe	Ile	Leu
				200					205					210
Val	Gly	Pro	Leu	Cys	Leu	Val	Leu	Val	Ser	Tyr	Ser	His	Ile	Leu
				215					220					225
Gly	Gly	Ile	Leu	Arg	Ile	Gln	Ser	Gly	Glu	Gly	Arg	Arg	Lys	Ala
				230					235					240
Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Cys	Val	Val	Gly	Leu	Phe	Phe
				245					250					255
Gly	Ser	Ala	Ile	Val	Met	Tyr	Met	Ala	Pro	Lys	Ser	Arg	His	Pro
				260					265					270
Glu	Glu	Gln	Gln	Lys	Val	Leu	Phe	Leu	Ile	Leu	Gln	Phe	Leu	Ser
				275					280					285
Thr	Pro	Met	Leu	Lys	Pro	Pro	Asp	Leu	Gln	Pro				
				290					295					

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 2185 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCACTATAGG	GCGAATTGGG	TACGGGCCCC	CCCTCGAGGT	CGACGGTATC	GATAAGCTTG	60
ATATCGAATT	CGGCACGAGC	CGGGCTCGGA	GAGGTGACGG	AACCGGGGCT	GGTAGCATAG	120
TTTGATTTGA	TGATGGAGCC	AACACAGGGG	TTGGAGCTGG	TACCGGTGAA	GCTGAGGCTA	180
AAAAGGTTCC	TGGAGTAGAC	GATGGAGCCA	TAAGTGAAC	CGGAGTCTGT	GAATGAAGCC	240
AGGACAGGAG	CAGCACCTGG	CGATGGTGCC	AGGACCGGAA	GAGGAGCCAG	AGGAGGAGCT	300
GGAGAAGGAG	CCAGAATTGC	TGTCTGTGGA	GCCGCCATAG	GAGCCAGAGG	GGTGGCTAGA	360
GCCTGAGAAT	GCAGAAGATG	CTGGAGCCAG	AAGGGAAGCC	TGAGCTGGAG	CTGGATTGTTG	420
TGCTGACGGA	AAAGGACTGG	CCAGAGCCGA	AGCTGGCACC	AGGGACAGGT	GAGCATTCTG	480
GGGCCACGGT	TGAGTTCAAC	CCACTGACTT	CAGGTGAAGG	ACTGTGGACC	AGCTTGAGAA	540
GAGGCCTCAC	CAGAGTGGGT	GTGGGGCATG	GGGGCTCGAG	CAGTACCCAG	AGTAGGTGTG	600
GGTAGCCCGG	CCAGGGGTTA	ACGTGGGGCG	TGGATTCAAC	ACAGCTTGGA	AGCCCAGAGC	660
TGGGAGGCCC	GGGTGCTTGG	GCCAATTGAG	GAACAGGAGT	CAGTCCATCC	CGAGGGGGTT	720
GTCTCACTAC	AATCTTCACA	CGCCTTTATT	ATTCAACATG	GTTGGTGGCA	CCTGGTTAGC	780
AGCAAGCGGA	AGGCTGAGGC	CAGTAGGGGC	AGGGGTGTTA	CTGGGGGTCTG	AAGAAGCCAG	840
CACAGAGACT	GGGTAGGGC	CAGGGGTCGG	GGCCACGGCC	TGGATGAGGC	CCACATGGGC	900
AGGCTGGCTG	ATGAGATGGT	GCTGCCCCCC	TGCTGACACG	AGGTGCACCA	CATTCTTTTG	960

CAGCGGGCGG	GCTGCCCCAC	AGCAAGCTGG	CGCACCTGGG	CACCATCCAA	AATACAGCTT	1020
GTTTCCCTGG	ATTTGGAAGG	TGAGAGGTTT	GCTTCCCCCT	CCATTAACCA	CTGACGTTGT	1080
GCCAGTGAGA	CTAACTCTCC	GCGCCAATCT	GTCCGCGGGT	GACCTCCTTC	GCGGGCGTGG	1140
CCTACCTCTT	CCTCATGTTT	CACACTGTCC	CCGCACAGCC	CGACTTTTAC	TTGAGGGCTG	1200
GTTTCTGCGG	CAGGGCTTGC	TGGACACAAA	CCTCACTGCG	TCGGTGGCCA	CACTGCTGGC	1260
CATCGCCGTG	GAGCGGCACC	GCAGTGTGAT	GGCCGTGCAG	CTGCACAGCC	GCCTGCCCCG	1320
TGGCCGCGTG	GTCATGCTCA	TTGTGGGCGT	GTGGGTGGCT	GCCCTGGGCG	TGGGCTGCT	1380
GCCTGCCCCA	TCCTGGCACT	GCCTCTGTGC	CCTGGACCGC	TCCTCACGCA	TGGCACCCCT	1440
GCTCAGCCCG	TCCTATTTGG	CCGTCTGGGC	TCTGTCGAGC	CTGCTTGTCT	TCCTGCTCAT	1500
GGTGGCTGTG	TACACCCGCA	TTTCTTCTA	CGTGCGGCGG	CGAGTGCAGC	GCATGGCAGA	1560
GCATGTCAGC	TGCCACCCCC	GCTACCGAGA	GACCACGCTC	AGCCTGGTCA	AGACTGTTGT	1620
CATCATCCTG	GGGGCGTTTC	TGGTCTGCTG	GACACCAGGC	CAGGTGGTAC	TGCTCCTGGA	1680
TGGTTTAGGC	TGTGAGTCCT	GCAATGTCCT	GGCGTTAGAA	AAGTACTTCC	TACTGTTGGC	1740
CGAGCCAACC	TCACTGGTCA	ATGCTGCTGT	GTACTCTTGC	CGAGATGCTG	AGATGCGCCG	1800
CACCTTCCGC	CGCCTTCTCC	TGCTGCGCGT	GCCTCCGCCA	GTCCACCCGC	GAGTCTGTCC	1860
ACTATACATC	CTCTGCCCAG	GGAGGTGCCA	GCACTCGCAT	CATGCTTCCC	GAGAACGGCC	1920
ACCCACTGAT	GGACTCCACC	CTTAGCTAC	CTTGAACCTAC	AGCGGTACGC	GGCAAGCAAC	1980
AAATCCACAG	CCCCTGATGA	CTTGTGGGTG	CTCCTGGCTC	AACCCAACCT	CGTGCCGAAT	2040
TCCTGCAGCC	CGGGGGATCC	ACTAGTTCTA	GAGCGGCGCC	ACCGCGGTGG	AGCTCCAGCT	2100
TTTGTTCCTT	TTAGTGAGGG	TTAATTTCTA	GCTTGGCGTA	ATCATGGTCA	TAGCTGTTTC	2160
CTGTGTGAAA	TTGTTATCCG	CTCAC				2185

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 393 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS:
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Pro	Thr	Trp	Ala	Gly	Trp	Leu	Met	Arg	Trp	Cys	Cys	Pro
				5					10					15
Pro	Ala	Asp	Thr	Arg	Cys	Thr	Thr	Phe	Leu	Cys	Ser	Gly	Arg	Ala
				20					25					30
Ala	Pro	Gln	Gln	Ala	Gly	Ala	Pro	Gly	His	His	Pro	Lys	Tyr	Ser
				35					40					45
Leu	Phe	Pro	Trp	Ile	Trp	Lys	Val	Arg	Gly	Leu	Leu	Pro	Pro	Pro
				50					55					60
Leu	Thr	Thr	Asp	Val	Val	Pro	Val	Arg	Leu	Thr	Leu	Arg	Ala	Asn
				65					70					75
Leu	Ser	Ala	Ala	Asp	Leu	Leu	Arg	Gly	Arg	Gly	Leu	Pro	Leu	Pro
				80					85					90
His	Val	Pro	His	Cys	Pro	Arg	Thr	Ala	Arg	Leu	Ser	Leu	Glu	Gly
				95					100					105
Trp	Phe	Leu	Arg	Gln	Gly	Leu	Leu	Asp	Thr	Asn	Leu	Thr	Ala	Ser
				110					115					120
Val	Ala	Thr	Leu	Leu	Ala	Ile	Ala	Val	Glu	Arg	His	Arg	Ser	Val
				125					130					135
Met	Ala	Val	Gln	Leu	His	Ser	Arg	Leu	Pro	Arg	Gly	Arg	Val	Val
				140					145					150
Met	Leu	Ile	Val	Gly	Val	Trp	Val	Ala	Ala	Leu	Gly	Leu	Gly	Leu
				155					160					165
Leu	Pro	Ala	His	Ser	Trp	His	Cys	Leu	Cys	Ala	Leu	Asp	Arg	Ser
				170					175					180

Ser	Arg	Met	Ala	Pro	Leu	Leu	Ser	Arg	Ser	Tyr	Leu	Ala	Val	Trp
				185					190					195
Ala	Leu	Ser	Ser	Leu	Leu	Val	Phe	Leu	Leu	Met	Val	Ala	Val	Tyr
				200					205					210
Thr	Arg	Ile	Phe	Phe	Tyr	Val	Arg	Arg	Arg	Val	Gln	Arg	Met	Ala
				215					220					225
Glu	His	Val	Ser	Cys	His	Pro	Arg	Tyr	Arg	Glu	Thr	Thr	Leu	Ser
				230					235					240
Leu	Val	Lys	Thr	Val	Val	Ile	Ile	Leu	Gly	Ala	Phe	Val	Val	Cys
				245					250					255
Trp	Thr	Pro	Gly	Gln	Val	Val	Leu	Leu	Leu	Asp	Gly	Leu	Gly	Cys
				260					265					270
Glu	Ser	Cys	Asn	Val	Leu	Ala	Leu	Glu	Lys	Tyr	Phe	Leu	Leu	Leu
				275					280					285
Ala	Glu	Pro	Thr	Ser	Leu	Val	Asn	Ala	Ala	Val	Tyr	Ser	Cys	Arg
				290					295					300
Asp	Ala	Glu	Met	Arg	Arg	Thr	Phe	Arg	Arg	Leu	Leu	Leu	Leu	Arg
				305					310					315
Val	Pro	Pro	Pro	Val	His	Pro	Arg	Val	Cys	Pro	Leu	Tyr	Ile	Leu
				320					325					330
Cys	Pro	Gly	Arg	Cys	Gln	His	Ser	His	His	Ala	Ser	Arg	Glu	Arg
				335					340					345
Pro	Pro	Thr	Asp	Gly	Leu	His	Pro	Leu	Ala	Thr	Leu	Asn	Tyr	Ser
				350					355					360
Gly	Thr	Arg	Gln	Ala	Thr	Asn	Pro	Gln	Pro	Leu	Met	Thr	Cys	Gly
				365					370					375
Cys	Ser	Trp	Leu	Asn	Pro	Thr	Ser	Cys	Arg	Ile	Pro	Ala	Ala	Arg
				380					385					390
Gly	Ile	His												

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 1474 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCACGAGC	ATAAGAAGAC	AGAGAGAACT	GAGTATCCTC	CCAAAGGTGA	CACTGGAAGC	60
AATGAACACC	ACAGTAATGC	AAGGCTTGAA	CAGATCTAAG	CGGTGCCCCA	AAGACACTCG	120
GATAGTACAG	CTGGTATTCC	CAGCCCTCTA	CACAGTGGTT	TTCTTGACCG	CAATCCTGCT	180
GAATACTTTG	GCTCTGTGGG	TGTTTGTTCA	CATCCCCAGC	TGGTCCACCT	TCATCATCTA	240
CCTCAAAAAC	ACTTTGGTGG	CCGACTTGAT	AATGACAGTG	ATGCTTCCTT	TCAAAATCCT	300
CTCTGACTCA	CACCTGGCAC	CCTGGCAGCT	CAGAGCTTTT	GTGTGTCGTT	TTTCTTCGGT	360
GATATTTTAT	GAGACCATGT	ATGTGGGCAT	AGTGCTGTTA	GGGCTCATAG	CCTTTGACAG	420
ATTCCTCAAG	ATCATCAGAC	CTTTGAGAAA	TATTTTTCTA	AAAAAACCTG	TTTGGGGAAA	480
AACGGTCTCA	ATCTTCATCT	GGTTCTTTTG	GTTCTTCATC	TCCCTGCCAA	ATATGATCTT	540
GAGCAACAAG	GAAGCAACAC	CATCGTCTGT	GAAAAAGTGT	GCTTCCTTAA	AGGGGCCTCT	600
GGGGCTGAAA	TGGCATCAAA	TGGTAAATAA	CATATGCCAG	TTTATTTTCT	GGACTGTTTT	660
TATCCTAATG	CTTGTGTTTT	ATGTGGTTAT	TGCAAAAAAG	TATATGATTG	TTATAGAAAG	720
TCCAAAAGTA	AGGACAGAAA	AAACAACAAA	AAGCTGGAAG	GCAAAGTATT	TGTTGTCGTG	780

GCTGTCTTCT	TTGTGTGTTT	TGCTCCATTT	CATTTCGCCA	GAGTTCCATA	TACTCACAGT	840
CAAACCAACA	ATAAGACTGA	CTGTAGACTG	CAAAATCAAC	TGTTTATTGC	TAAAGAAACA	900
ACTCTCTTTT	TGGCAGCAAC	TAACATTTGT	ATGGATCCCT	TAATATACAT	ATTCTTATGT	960
AAAAAATTCA	CAGAAAAGCT	ACCATGTATG	CAAGGGAGAA	AGACCACAGC	ATCAAGCCAA	1020
GAAAATCATA	GCAGTCAGAC	AGACAACATA	ACCTTAGGCT	GACAACTGTA	CATAGGGGTA	1080
ACTTCTATTT	ATTGATGAGA	CTTCCGTAGA	TAATGTGGAA	ATCCAATTTA	ACCAAGAAAA	1140
AAAGATTGGG	GCAAATGCTC	TCTTACATTT	TATTATCCTG	GTGTACAGAA	AAGATTATAT	1200
AAAATTTAAA	TCCACATAGA	TCTATTCATA	AGCTGAATGA	ACCATTACTA	AGAGAATGCA	1260
ACAGGATACA	AATGGCCACT	AGAGGTCATT	ATTTGTTTCT	TTCTTTCTTT	TTTTTTTTTT	1320
AATTTCAAGA	GCATTTCACT	TTAACATTTT	GGAAAAGACT	AAGGAGAAAC	GTATATCCCT	1380
ACAAACCTCC	CCTCCAAACA	CCTTCTTACA	TTCTTTTCCA	CAATTCACAT	AACACTACTG	1440
CTTTTGTGCC	CCTTAAATGT	AGATTTGTTG	GCTG			1474

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 293 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS:
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asn	Thr	Thr	Val	Met	Gln	Gly	Phe	Asn	Arg	Ser	Lys	Arg	Cys
				5					10					15
Pro	Lys	Asp	Thr	Arg	Ile	Val	Gln	Leu	Val	Phe	Pro	Ala	Leu	Tyr
				20					25					30
Thr	Val	Val	Phe	Leu	Thr	Gly	Ile	Leu	Leu	Asn	Thr	Leu	Ala	Leu
				35					40					45
Trp	Val	Phe	Val	His	Ile	Pro	Ser	Ser	Ser	Thr	Phe	Ile	Ile	Tyr
				50					55					60
Leu	Lys	Asn	Thr	Leu	Val	Ala	Asp	Leu	Ile	Met	Thr	Leu	Met	Leu
				65					70					75
Pro	Phe	Lys	Ile	Leu	Ser	Asp	Ser	His	Leu	Ala	Pro	Trp	Gln	Leu
				80					85					90
Arg	Ala	Phe	Val	Cys	Arg	Phe	Ser	Ser	Val	Ile	Phe	Tyr	Glu	Thr
				95					100					105
Met	Tyr	Val	Gly	Ile	Val	Leu	Leu	Gly	Leu	Ile	Ala	Phe	Asp	Arg
				110					115					120
Phe	Leu	Lys	Ile	Ile	Arg	Pro	Leu	Arg	Asn	Ile	Phe	Leu	Lys	Lys
				125					130					135
Pro	Val	Trp	Gly	Lys	Thr	Val	Ser	Ile	Phe	Ile	Trp	Phe	Phe	Trp
				140					145					150
Phe	Phe	Ile	Ser	Leu	Pro	Asn	Met	Ile	Leu	Ser	Asn	Lys	Glu	Ala
				155					160					165
Thr	Pro	Ser	Ser	Val	Lys	Lys	Cys	Ala	Ser	Leu	Lys	Gly	Pro	Leu
				170					175					180
Gly	Leu	Lys	Trp	His	Gln	Met	Val	Asn	Asn	Ile	Cys	Gln	Phe	Ile
				185					190					195
Phe	Trp	Thr	Val	Phe	Ile	Leu	Met	Leu	Val	Phe	Tyr	Val	Val	Ile
				200					205					210
Ala	Lys	Lys	Tyr	Met	Ile	Leu	Ile	Glu	Ser	Pro	Lys	Val	Arg	Thr
				215					220					225
Glu	Lys	Thr	Thr	Lys	Ser	Trp	Lys	Ala	Lys	Tyr	Leu	Leu	Ser	Trp

	230		235		240
Leu Ser Ser Leu	Cys Val Leu Leu His	Phe Ile Ser Pro Glu	Phe		
	245		250		255
His Ile Leu Thr	Val Lys Pro Thr Ile	Arg Leu Thr Val Asp	Cys		
	260		265		270
Lys Ile Asn Cys	Leu Leu Leu Lys Lys	Gln Leu Ser Phe Trp	Gln		
	275		280		285
Gln Leu Thr Phe	Val Trp Ile Pro				
	290				

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 1301 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTGGGTAT	TTCTGAGAAA	AAGGAAATAT	TTATAAAACC	ATCCAAAGAT	CCAGATAATT	60
TGCAAATAAA	TTGGAGGTTA	TAGAGGTTAT	AATCTGAATC	CCAAAGGAGA	CTGCAGCTGA	120
TGAAAGTGCT	TCCAAACTGA	AAATTGGACG	TGCCTTTACG	ATGGTAAGCG	TTAACAGCTC	180
CCACTGCTTC	TATAATGACT	CCTTTAAGTA	CACTTTGTAT	GGGTGCATGT	TCAGCATGGT	240
GTTTGTGCTT	GGGTTAATAT	CCAATTGTGT	TGCCATATAC	ATTTTCATCT	GCGTCCTCAA	300
AGTCCGAAAT	GAAACTACAA	CTTACATGAT	TAACCTGGCA	ATGTCAGACT	TGCTTTTTGT	360
TTTTACTTTA	CCCTTCAGGA	TTTTTTACTT	CACAACACGG	AATTGGCCAT	TTGGAGATTT	420
ACTTTGTAAG	ATTTCTGTGA	TGCTGTTTTA	TACCAACATG	TACGGAAGCA	TTCTGTTCTT	480
AACCTGTATT	AGTGTAGATC	GATTTCTGGC	AATTGTCTAC	CCATTTAAGT	CAAAGACTCT	540
AAGAACCAA	AGAAATGCAA	AGATTGTTTG	ACATGGCGTG	TGGTTAACTG	TGATCGGAGG	600
AAGTGCACCC	GCCGTTTTTG	TTCAGTCTAC	CCACTCTCAG	GGTAACAATG	CCTCAGAAGC	660
CTGCTTTGAA	AATTTTCCAG	AAGCCACATG	GAAAACATAT	CTCTCAAGGA	TTGTAATTTT	720
CATCGAAATA	GTGGGATTTT	TTATTCCTCT	AATTTTAAAT	GTAACCTGTT	CTAGTATGGT	780
GCTAAAAATG	TTAACCAAAC	CTGTTACATT	AAGTAGAAGC	AAAATAAACA	AAACTAAGGT	840
TTTAAAAATG	ATTTTGTAC	ATTTGATCAT	ATTCTGTTTC	TGTTTTGTTC	CTTACAATAT	900
CAATCTTATT	TTATATTCTC	TTGTGAGAAC	ACAAACATTT	GTTAATTGCT	CAGTAGTGGC	960
AGCAGTAAGG	ACAATGTACC	CAATCACTCT	CTGTATTGCT	GTTTCCAAGT	GTTGTTTTGA	1020
CCCTATAGTT	TACTACTTTA	CATCGGACAC	AATTCAGAAT	TCAATAAAAA	TGAAAACTG	1080
GTCTGTCAGG	AGAAGTGACT	TCAGATTCTC	TGAAGTTCAT	GGTGCAGAGA	ATTTTATTCA	1140
GCATAACCTA	CAGACCTTAA	AAAGTAAGAT	ATTTGACAAT	GAATCTGCTG	CCTGAAATAA	1200
AACCATTAGG	ACTCACTGGG	ACAGAACTTT	CAAGTTCCTT	CAACTGTGAA	AAGTGTCTTT	1260
TTGGACAAAC	TATTTTTTCCA	CCTCCAAAAG	AAATTAACAC	A		1301

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 344 AMINO ACIDS  
 (B) TYPE: AMINO ACID  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Val Ser Val Asn Ser Ser His Cys Phe Tyr Asn Asp Ser Phe

Lys Tyr Thr Leu	5	Tyr Gly Cys Met Phe	10	Ser Met Val Phe Val	15
	20		25		30
Gly Leu Ile Ser	35	Asn Cys Val Ala Ile	40	Tyr Ile Phe Ile Cys	45
Leu Lys Val Arg	50	Asn Glu Thr Thr Thr	55	Tyr Met Ile Asn Leu	60
Met Ser Asp Leu	65	Leu Phe Val Phe Thr	70	Leu Pro Phe Arg Ile	75
Tyr Phe Thr Thr	80	Arg Asn Trp Pro Phe	85	Gly Asp Leu Leu Cys	90
Ile Ser Val Met	95	Leu Phe Tyr Thr Asn	100	Met Tyr Gly Ser Ile	105
Phe Leu Thr Cys	110	Ile Ser Val Asp Arg	115	Phe Leu Ala Ile Val	120
Pro Phe Lys Ser	125	Lys Thr Leu Arg Thr	130	Lys Arg Asn Ala Lys	135
Val Cys Thr Gly	140	Val Trp Leu Thr Val	145	Ile Gly Gly Ser Ala	150
Ala Val Phe Val	155	Gln Ser Thr His Ser	160	Gln Gly Asn Asn Ala	165
Glu Ala Cys Phe	170	Glu Asn Phe Pro Glu	175	Ala Thr Trp Lys Thr	180
Leu Ser Arg Ile	185	Val Ile Phe Ile Glu	190	Ile Val Gly Phe Phe	195
Pro Leu Ile Leu	200	Asn Val Thr Cys Ser	205	Ser Met Val Leu Lys	210
Leu Thr Lys Pro	215	Val Thr Leu Ser Arg	220	Ser Lys Ile Asn Lys	225
Lys Val Leu Lys	230	Met Ile Phe Val His	235	Leu Ile Ile Phe Cys	240
Cys Phe Val Pro	245	Tyr Asn Ile Asn Leu	250	Ile Leu Tyr Ser Leu	255
Arg Thr Gln Thr	260	Phe Val Asn Cys Ser	265	Val Val Ala Ala Val	270
Thr Met Tyr Pro	275	Ile Thr Leu Cys Ile	280	Ala Val Ser Asn Cys	285
Phe Asp Pro Ile	290	Val Tyr Tyr Phe Thr	295	Ser Asp Thr Ile Gln	300
Ser Ile Lys Met	305	Lys Asn Trp Ser Val	310	Arg Arg Ser Asp Phe	315
Phe Ser Glu Val	320	His Gly Ala Glu Asn	325	Phe Ile Gln His Asn	330
Gln Thr Leu Lys	335	Ser Lys Ile Phe Asp	340	Asn Glu Ser Ala Ala	

- (2) INFORMATION FOR SEQ ID NO:9:
- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 30 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR



(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: 30  
 GACTAAAGCT TAATGAGTAG TGAAATGGTG

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 31 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: 31  
 GAACTTCTAG ACCCTCAGGG TTGTAAATCA G

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 30 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11: 30  
 GACTAAAGCT TAATGAGGCC CACATGGGCA

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 32 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: 32  
 GAACTTCTAG ACGAACTAGT GGATCCCCC GG

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 30 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: 30  
 GACTAAAGCT TAATGGCGTC TTTCTCTGCT

- (2) INFORMATION FOR SEQ ID NO:14:
- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 30 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:  
 GAACTTCTAG ACTTCACACA GTTGTACTAT 30
- (2) INFORMATION FOR SEQ ID NO:15:
- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 30 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:  
 GACTAAAGCT TAATGGTAAG CGTTAACAGC 30
- (2) INFORMATION FOR SEQ ID NO:16:
- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 31 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:  
 GAACTTCTAG ACTTCAGGCA GCAGATTCAT T 31
- (2) INFORMATION FOR SEQ ID NO:17:
- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 34 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE  
 (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:  
 GTCCAAGCTT GCCACCATGA GTAGTGAAAT GGTG 34
- (2) INFORMATION FOR SEQ ID NO:18:
- (i) SEQUENCE CHARACTERISTICS  
 (A) LENGTH: 58 BASE PAIRS  
 (B) TYPE: NUCLEIC ACID  
 (C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAGGGTTGT AAATCAGG 58

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 34 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GTCCAAGCTT GCCACCATGG TTGGTGGCAC CTGG 34

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 58 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAGTGGATC CCCC GTGC 58

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 34 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GTCCAAGCTT GCCACCATGA ACACCACAGT AATG 34

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS

(A) LENGTH: 61 BASE PAIRS

(B) TYPE: NUCLEIC ACID

(C) STRANDEDNESS: SINGLE

(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAAGGGATC CATACAAATG 60  
T 61

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 34 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTCCAAGCTT GCCACCATGG TAAGCGTTAA CAGC

34

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 61 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTAGCTCGAG TCAAGCGTAG TCTGGGACGT CGTATGGGTA GCAGGCAGCA GATTCATTGT 60  
C 61

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 30 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGGGATCCCT CCATGAGTAG TGAAATGGTG

30

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS

- (A) LENGTH: 29 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CGGGATCCCG CTCAGGGTTG TAAATCAGG

29